

asterisks represent residues with potential roles in deacetylase activity.

FIGURE 4 displays the amino acid sequence alignment of AtHD2A (SEQ ID NO:6), AtHD2B (SEQ ID NO:8) and maize HD2 (ZmHD2; SEQ ID NO:14). Identical amino acids are shaded in black. The amino acids with asterisks are the predicted histone deacetylase catalytic residues. The extended acidic domains are underlined.

IN THE CLAIMS:

Please cancel claims 4, 29 and 30 without prejudice to or disclaimer of the subject matter contained therein.

Please replace claims 1 and 9 as follows:

(Twice Amended) A method of repressing transcription of a coding sequence of interest in a transgenic plant, comprising:

a) introducing into a plant:

i) a first chimeric nucleotide sequence comprising a first regulatory element in operative association with a gene of interest, and a controlling sequence; and

ii) a second chimeric nucleotide sequence comprising a second regulatory element in operative association with a nucleotide sequence encoding a histone deacetylase fused with a DNA binding protein, said DNA binding protein interacting with said controlling sequence, to produce said transgenic plant; and

b) growing said transgenic plant;

wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of:

AtRPD3A, a nucleotide sequence that hybridizes to *AtRPD3A* under a hybridization condition,

AtRPD3B, a nucleotide sequence that hybridizes to *AtRPD3B* under a hybridization condition,

AtHD2A, a nucleotide sequence that hybridizes to *AtHD2A* under a hybridization condition,

AtHD2B, a nucleotide sequence that hybridizes to *AtHD2B* under a hybridization condition,

nucleotides 1-1807 of SEQ ID NO:1, a nucleotide sequence that hybridizes to nucleotides 1-1807 of SEQ ID NO:1 under a hybridization condition,

nucleotides 142-1644 of SEQ ID NO:1, a nucleotide sequence that hybridizes to nucleotides 142-1644 of SEQ ID NO:1 under a hybridization condition,

nucleotides 1-1800 of SEQ ID NO:3, a nucleotide sequence that hybridizes to nucleotides 1-1800 of SEQ ID NO:3 under a hybridization condition,

nucleotides 121-1533 of SEQ ID NO:3, a nucleotide sequence that hybridizes to nucleotides 121-1533 of SEQ ID NO:3 under a hybridization condition,

nucleotides 1-939 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 1-939 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-783 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-783 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-681 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-681 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-534 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-534 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-267 and 457-534 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-267 and 457-534 of SEQ ID NO:5 under a hybridization condition,

nucleotides 1-1212 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 1-1212 of SEQ ID NO:7 under a hybridization condition,

nucleotides 61-975 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 61-975 of SEQ ID NO:7 under a hybridization condition,

nucleotides 61-855 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 61-855 of SEQ ID NO:7 under a hybridization condition,

nucleotides 61-655 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 61-655 of SEQ ID NO:7 under a hybridization condition,

nucleotides 61-276 and 522-655 of SEQ ID NO:7, and a nucleotide sequence that hybridizes to nucleotides 61-276 and 522-655 of SEQ ID NO:7 under a hybridization condition;

wherein each said hybridization condition is selected from the group consisting of:

hybridization in 4XSSC at 65°C, followed by washing in 0.1XSSC at 65°C for an hour,

hybridization in 50% formamide and 4XSSC at 42°C, followed by washing in 0.1XSSC at 65°C for an hour, and

hybridization in 0.5 M Na₂HPO₄ (pH 7.2), 7% SDS, and 1mM EDTA at 65°C, followed by washing for 15 minutes in 2 x SSC with 0.1% SDS at room temperature, then washing twice for 20 minutes in 0.1 x SSC, 0.1% SDS at 65°C; and

wherein said nucleotide sequence that hybridizes encodes a product that exhibits repression of gene expression activity.

(Twice Amended) An isolated nucleotide sequence, selected from the group consisting of:

- i) SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7,

ii) a nucleotide sequence that hybridizes to SEQ ID NO:3, SEQ ID NO:5,
or SEQ ID NO:7,

iii) a nucleotide sequence that hybridizes to nucleotides 1-1800 of SEQ ID
NO:3 under a hybridization condition,

iv) nucleotides 121-1533 of SEQ ID NO:3,

v) a nucleotide sequence that hybridizes to nucleotides 121-1533 of SEQ
ID NO:3 under a hybridization condition,

vi) nucleotides 1-939 of SEQ ID NO:5,

vii) a nucleotide sequence that hybridizes to nucleotides 1-939 of SEQ ID
NO:5 under a hybridization condition,

viii) nucleotides 49-783 of SEQ ID NO:5,

ix) a nucleotide sequence that hybridizes to nucleotides 49-783 of SEQ ID
NO:5 under a hybridization condition,

x) nucleotides 49-681 of SEQ ID NO:5,

xi) a nucleotide sequence that hybridizes to nucleotides 49-681 of SEQ ID
NO:5 under a hybridization condition,

xii) nucleotides 49-534 of SEQ ID NO:5,

xiii) a nucleotide sequence that hybridizes to nucleotides 49-534 of SEQ ID
NO:5 under a hybridization condition,

xiv) nucleotides 49-267 and 457-534 of SEQ ID NO:5,

xv) a nucleotide sequence that hybridizes to nucleotides 49-267 and 457-
534 of SEQ ID NO:5 under a hybridization condition,

xvi) nucleotides 1-1212 of SEQ ID NO:7,

xvii) a nucleotide sequence that hybridizes to nucleotides 1-1212 of SEQ ID
NO:7 under a hybridization condition,

- xviii) nucleotides 61-975 of SEQ ID NO:7,
- xix) a nucleotide sequence that hybridizes to nucleotides 61-975 of SEQ ID NO:7 under a hybridization condition,
- xx) nucleotides 61-855 of SEQ ID NO:7,
- xxi) a nucleotide sequence that hybridizes to nucleotides 61-855 of SEQ ID NO:7 under a hybridization condition,
- xxii) nucleotides 61-655 of SEQ ID NO:7,
- xxiii) a nucleotide sequence that hybridizes to nucleotides 61-655 of SEQ ID NO:7 under a hybridization condition,
- xxiv) nucleotides 61-276 and 522-655 of SEQ ID NO:7, and
- xxv) a nucleotide sequence that hybridizes to nucleotides 61-276 and 522-655 of SEQ ID NO:7 under a hybridization condition;

wherein each said hybridization condition is selected from the group consisting of:

hybridization in 4XSSC at 65°C, followed by washing in 0.1XSSC at 65°C for an hour,

hybridization in 50% formamide and 4XSSC at 42°C, followed by washing in 0.1XSSC at 65°C for an hour, and

hybridization in 0.5 M Na_2HPO_4 (pH 7.2), 7% SDS, and 1 mM EDTA at 65°C, followed by washing for 15 minutes in 2 x SSC with 0.1% SDS at room temperature, then twice washing for 20 minutes in 0.1 x SSC, 0.1% SDS at 65°C; and

wherein said nucleotide sequence that hybridizes encodes a product that exhibits repression of gene expression activity.

Please add new claims 32-56 as follows:

--32. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: AtRPD3A, AtRPD3B, AtHD2A, and AtHD2B.--

--33. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of nucleotides 1-1807 of SEQ ID NO:1 and nucleotides 142-1644 of SEQ ID NO:1.--

--34. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: nucleotides 1-1800 of SEQ ID NO:3 and nucleotides 121-1533 of SEQ ID NO:3.--

--35. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: nucleotides 1-939 of SEQ ID NO:5; nucleotides 49-783 of SEQ ID NO:5; nucleotides 49-681 of SEQ ID NO:5; and nucleotides 49-534 of SEQ ID NO:5.--

--36. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: nucleotides 1-1212 of SEQ ID NO:7; nucleotides 61-975 of SEQ ID NO:7; nucleotides 61-855 of SEQ ID NO:7; and nucleotides 61-655 of SEQ ID NO:7.--

--37. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide sequence that hybridizes to AtRPD3A, a nucleotide sequence that hybridizes to AtRPD3B, a nucleotide sequence that hybridizes to AtHD2A, and a nucleotide sequence that hybridizes to AtHD2B.--

--38. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide sequence that hybridizes to

nucleotides 1-1807 of SEQ ID NO:1 and a nucleotide sequence that hybridizes to nucleotides 142-1644 of SEQ ID NO:1.--

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--39. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide sequence that hybridizes to nucleotides 1-1800 of SEQ ID NO:3 and a nucleotide sequence that hybridizes to nucleotides 121-1533 of SEQ ID NO:3.--

--40. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide sequence that hybridizes to nucleotides 1-939 of SEQ ID NO:5; a nucleotide sequence that hybridizes to nucleotides 49-783 of SEQ ID NO:5; a nucleotide sequence that hybridizes to nucleotides 49-681 of SEQ ID NO:5; and a nucleotide sequence that hybridizes to nucleotides 49-534 of SEQ ID NO:5.--

--41. The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide sequence that hybridizes to nucleotides 1-1212 of SEQ ID NO:7; a nucleotide sequence that hybridizes to nucleotides 61-975 of SEQ ID NO:7; a nucleotide sequence that hybridizes to nucleotides 61-855 of SEQ ID NO:7; and a nucleotide sequence that hybridizes to nucleotides 61-655 of SEQ ID NO:7.--

--42. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises SEQ ID NO:3.--

--43. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises SEQ ID NO:5.--

--44. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises SEQ ID NO:7.--

--45. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 121-1533 of SEQ ID NO:3.--

--46. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 1-939 of SEQ ID NO:5.--

--47. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 49-783 of SEQ ID NO:5.--

--48. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 49-681 of SEQ ID NO:5.--

--49. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 49-534 of SEQ ID NO:5.--

--50. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 49-267 and 457-534 of SEQ ID NO:5.--

--51. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 1-1212 of SEQ ID NO:7.--

--52. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 61-975 of SEQ ID NO:7.--

--53. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 61-975 of SEQ ID NO:7.--

--54. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 61-855 of SEQ ID NO:7.--

--55. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 61-655 of SEQ ID NO:7.--

--56. The isolated nucleotide sequences of claim 9, wherein said nucleotide sequence comprises nucleotides 61-276 of SEQ ID NO:7.--

REMARKS

Claims 1-3, 5-9, 11-19 and 31-56 are pending. By the Office Action, the drawings are objected to; the specification is objected to; claims 1-9, 11-19, 29 and 30 are rejected; and